

SEQUENCE LISTING

<110> Ottawa Health Research Institute
 Megeney, Lynn

<120> MODULATION OF STEM CELL DIFFERENTIATION
 BY MODULATION OF CASPASE-3 ACTIVITY

<130> 241-137PCT

<140> N/A

<141> 2003-12-10

<150> US 60/431,991

<151> 2002-12-10

<150> US 60/431,990

<151> 2002-12-10

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 835

<212> DNA

<213> Homo sapiens

<220>

<221>

<222>

<223> human caspase-3 gene

<400> 1

```

aatggagaac actgaaaact cagtggattc aaaatocatt aaaaatttgg aaccaagat 60
catacatgga agcgaatcaa tggactctgg aatatccctg gacaacagtc ataaaatgga 120
ttatccctgag atgggtttat gtataataat taataataag aattttcata aaagcactgg 180
aatgacatct cggctctggtc cagatgtcga tgcagcnaac ctccagggaaa cattoagaaa 240
cttgaataat gaagtcagga ataaaaatga tcttacacgt gaagaaattg tgggaattgat 300
gcgatgatgtt totaaagaag atcacagcaa aaggagcagt tttgtttgtg tgettctgag 360
aatgggtgaa gaaggaataa tttttggaac aaatggacct gttgacctga aaaaaataac 420
aaactttttc agaggggacg gttgtagaag tctaactgga aaacccaaac ttttoattat 480
tcaggcctgc cgtggtacag aactggactg tggcattgag acagacagtg gtgttgatga 540
tgacatggcg tgtcataaaa taccagtggg ggcogacttc ttgtatgcat actccacagc 600
acctggttat tattcttggc gaaattcaaa ggatgggtcc tgggttoatc agtcgctttg 660
tgccatgctg aaacagtatg ccgacaagct tgaatttatg cacattctta cccgggttaa 720
ccgaaagggtg gcaacagaat ttgagtcott ctcttttgac gctacttttc atgcaaaaga 780
acagattoca tgtattgttt ccattgotcac aaaagaaactc tatttttacc actaa 835

```

<210> 2

<211> 277

<212> PRT

<213> Homo sapiens

BEST AVAILABLE COPY

<400> 2
Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu
1 5 10 15
Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
20 25 30
Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
35 40 45
Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
50 55 60
Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
65 70 75 80
Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
85 90 95
Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
100 105 110
Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
115 120 125
Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
130 135 140
Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
145 150 155 160
Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
165 170 175
Gly Val Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
180 185 190
Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
195 200 205
Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
210 215 220
Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
225 230 235 240
Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
245 250 255
His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
260 265 270
Leu Tyr Phe Tyr His
275

<210> 3
<211> 1910
<212> DNA
<213> Homo sapiens

<220>
<221>
<222>
<223> human MST1 gene

<400> 3
ccgggtgctg gcacgcggcga tggagacggg acagctgagg aaccgcgcgc gccggcagct 60
gaaaaagttg gatgaagata gtttaaccac acaaccagaa gaagtatttg atgtcttaga 120
gaaacttgga gaagggtcct atggcagcgt atacaaagct attcataaag agaccggcca 180
gattgttgct attaagcaag ttcctgtgga atcagaactc caggagataa tcaaagaaat 240

BEST AVAILABLE COPY

```

ctctataatg cagcaatgtg acagocctca tctagtcaaa tattatggca gttattttaa 300
gaacacagac ttatggatcg ttatggagta ctgtggggct gggtctgtat ctgatatcat 360
tcgattaaga aataaaacgt taacagaaga tgaatatagct acaatattac aatcaactct 420
taagggactt gaataccttc attttatgag aaaaatacac cgagatatca aggcaggaaa 480
tattttgcta aatacagaag gacatgcaaa acttgcagat ttgggggtag cagggtcaact 540
tacagatacc atggccaago ggaataoagt gataggaaca coattttgga tggotccaga 600
agtgattcag gaaattggat acaactgtgt agcagacatc tggtccttgg gaataactgc 660
catagaaatg gctgaaggaa agcgccttca tgcctgatato catccaatga gggcaatcct 720
catgattcct acaaatcctc ctccacatt ccgaaaacca gagctatggg cagataactt 780
tacagatttt gtgaaacagt gtcttgtaaa gagccctgag cagagggcca cagccactca 840
gctcctgcag caccattttg toaggagtgo caaaggagtg tcaatactgc gagacttaat 900
taatgaagcc atggatgtga aactgaaacg ccagggaatcc cagcagcggg aaatggacca 960
ggcgatgaa gaaaactcag aagaggatga aatggattct ggcaogattg ttcgagcagt 1020
gggtgatgag atgggcactg tccgagtagc cagcaaccatg actgatggag coataactat 1080
gattgagcac gatgacacgt tgcacacaca actgggcaac atgggtgatca atgcagagga 1140
tgagggaagag gaaggaaacta tgaagaagag ggatgagacc atgcagcctg cgaaccatc 1200
ctttcttgaa tattttgaaa aaaaagaaaa ggaaaaccag atcaacagct ttggcaagag 1260
tgtacctggg ccaactgaaa attcttcaga ttggaaaata ccacaggatg gagactacga 1320
gtttcttaag agttggacag tggaggacct tcagaagagg ctcttggccc tggaccccat 1380
gatggagcag gagattgaag agatccggca gaagtaccag tccaagcggc agcccatcct 1440
ggatgccata gaggctaaga agagacggca acaaaaactt tgagcaaggc caggctgtga 1500
gggcccagc tccaccaggg ctttgggtga attctggatg gottgtocat gtttgttagc 1560
cagcaccttc tgcctctgct tctctccaca gcaactttgt gaactcagga atgtgcgcga 1620
gtgggaaggg ctctcttgac agtcagcgtg ccactctgat gtgtgtatgt acattgggtca 1680
ggtatattat ctcaaaggat ttatatggg ogacttttaa ctcagagttt taaccaccag 1740
gaacagagac tctagttga gtgatagutg ggaaagtctt acattgtctg ttttcttct 1800
cccaatagot ttcaattggt ctctctggaa gaacttttaa aaaatataaa tatgcataa 1860
tatatatata ttataaatag atcccccaog caggttgggt gcatctctgt 1910

```

<210> 4

<211> 487

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Glu Thr Val Gln Leu Arg Asn Pro Pro Arg Arg Gln Leu Lys Lys
1          5          10          15
Leu Asp Glu Asp Ser Leu Thr Lys Gln Pro Glu Glu Val Phe Asp Val
20          25          30
Leu Glu Lys Leu Gly Glu Gly Ser Tyr Gly Ser Val Tyr Lys Ala Ile
35          40          45
His Lys Glu Thr Gly Gln Ile Val Ala Ile Lys Gln Val Pro Val Glu
50          55          60
Ser Asp Leu Gln Glu Ile Ile Lys Glu Ile Ser Ile Met Gln Gln Cys
65          70          75          80
Asp Ser Pro His Val Val Lys Tyr Tyr Gly Ser Tyr Phe Lys Asn Thr
85          90          95
Asp Leu Trp Ile Val Met Glu Tyr Cys Gly Ala Gly Ser Val Ser Asp
100          105          110
Ile Ile Arg Leu Arg Asn Lys Thr Leu Thr Glu Asp Glu Ile Ala Thr
115          120          125
Ile Leu Gln Ser Thr Leu Lys Gly Leu Glu Tyr Leu His Phe Met Arg
130          135          140
Lys Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Asn Thr Glu
145          150          155          160

```

BEST AVAILABLE COPY

Gly His Ala Lys Leu Ala Asp Phe Gly Val Ala Gly Gln Leu Thr Asp
 165 170 175
 Thr Met Ala Lys Arg Asn Thr Val Ile Gly Thr Pro Phe Trp Met Ala
 180 185 190
 Pro Glu Val Ile Gln Glu Ile Gly Tyr Asn Cys Val Ala Asp Ile Trp
 195 200 205
 Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Lys Arg Pro Tyr
 210 215 220
 Ala Asp Ile His Pro Met Arg Ala Ile Phe Met Ile Pro Thr Asn Pro
 225 230 235 240
 Pro Pro Thr Phe Arg Lys Pro Glu Leu Trp Ser Asp Asn Phe Thr Asp
 245 250 255
 Phe Val Lys Gln Cys Leu Val Lys Ser Pro Glu Gln Arg Ala Thr Ala
 260 265 270
 Thr Gln Leu Leu Gln His Pro Phe Val Arg Ser Ala Lys Gly Val Ser
 275 280 285
 Ile Leu Arg Asp Leu Ile Asn Glu Ala Met Asp Val Lys Leu Lys Arg
 290 295 300
 Gln Glu Ser Gln Gln Arg Glu Met Asp Gln Asp Asp Glu Glu Asn Ser
 305 310 315 320
 Glu Glu Asp Glu Met Asp Ser Gly Thr Met Val Arg Ala Val Gly Asp
 325 330 335
 Glu Met Gly Thr Val Arg Val Ala Ser Thr Met Thr Asp Gly Ala Asn
 340 345 350
 Thr Met Ile Glu His Asp Asp Thr Leu Pro Ser Gln Leu Gly Thr Met
 355 360 365
 Val Ile Asn Ala Glu Asp Glu Glu Glu Gly Thr Met Lys Arg Arg
 370 375 380
 Asp Glu Thr Met Gln Pro Ala Lys Pro Ser Phe Leu Glu Tyr Phe Glu
 385 390 395 400
 Gln Lys Glu Lys Glu Asn Gln Ile Asn Ser Phe Gly Lys Ser Val Pro
 405 410 415
 Gly Pro Leu Lys Asn Ser Ser Asp Trp Lys Ile Pro Gln Asp Gly Asp
 420 425 430
 Tyr Glu Phe Leu Lys Ser Trp Thr Val Glu Asp Leu Gln Lys Arg Leu
 435 440 445
 Leu Ala Leu Asp Pro Met Met Glu Gln Glu Ile Glu Glu Ile Arg Gln
 450 455 460
 Lys Tyr Gln Ser Lys Arg Gln Pro Ile Leu Asp Ala Ile Glu Ala Lys
 465 470 475 480
 Lys Arg Arg Gln Gln Asn Phe
 485

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 5

atgacatga ttacgaattc atggagacac

30

BEST AVAILABLE COPY

<210> 6
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 6
 cactotagat taattaaaaa aatagagttc

30

<210> 7
 <211> 268
 <212> PRT
 <213> Homo sapiens

<400> 7
 Ser Lys Ser Ile Lys Asn Leu Glu Pro Lys Ile Ile His Gly Ser Glu
 1 5 10 15
 Ser Met Asp Ser Gly Ile Ser Leu Asp Asn Ser Tyr Lys Met Asp Tyr
 20 25 30
 Pro Glu Met Gly Leu Cys Ile Ile Ile Asn Asn Lys Asn Phe His Lys
 35 40 45
 Ser Thr Gly Met Thr Ser Arg Ser Gly Thr Asp Val Asp Ala Ala Asn
 50 55 60
 Leu Arg Glu Thr Phe Arg Asn Leu Lys Tyr Glu Val Arg Asn Lys Asn
 65 70 75 80
 Asp Leu Thr Arg Glu Glu Ile Val Glu Leu Met Arg Asp Val Ser Lys
 85 90 95
 Glu Asp His Ser Lys Arg Ser Ser Phe Val Cys Val Leu Leu Ser His
 100 105 110
 Gly Glu Glu Gly Ile Ile Phe Gly Thr Asn Gly Pro Val Asp Leu Lys
 115 120 125
 Lys Ile Thr Asn Phe Phe Arg Gly Asp Arg Cys Arg Ser Leu Thr Gly
 130 135 140
 Lys Pro Lys Leu Phe Ile Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp
 145 150 155 160
 Cys Gly Ile Glu Thr Asp Ser Gly Val Asp Asp Asp Met Ala Cys His
 165 170 175
 Lys Ile Pro Val Glu Ala Asp Phe Leu Tyr Ala Tyr Ser Thr Ala Pro
 180 185 190
 Gly Tyr Tyr Ser Trp Arg Asn Ser Lys Asp Gly Ser Trp Phe Ile Gln
 195 200 205
 Ser Leu Cys Ala Met Leu Lys Gln Tyr Ala Asp Lys Leu Glu Phe Met
 210 215 220
 His Ile Leu Thr Arg Val Asn Arg Lys Val Ala Thr Glu Phe Glu Ser
 225 230 235 240
 Phe Ser Phe Asp Ala Thr Phe His Ala Lys Lys Gln Ile Pro Cys Ile
 245 250 255
 Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Tyr His
 260 265

<210> 8
 <211> 249

BEST AVAILABLE COPY

<212> PRT

<213> Homo sapiens

<400> 8

```

Ser Gly Ile Ser Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met
 1           5           10           15
Gly Leu Cys Ile Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly
          20           25           30
Met Thr Ser Arg Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu
          35           40           45
Thr Phe Arg Asn Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr
          50           55           60
Arg Glu Glu Ile Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His
65           70           75           80
Ser Lys Arg Ser Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu
          85           90           95
Gly Ile Ile Phe Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr
          100          105          110
Asn Phe Phe Arg Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys
          115          120          125
Leu Phe Ile Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile
          130          135          140
Glu Thr Asp Ser Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro
145          150          155          160
Val Glu Ala Asp Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr
          165          170          175
Ser Trp Arg Asn Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys
          180          185          190
Ala Met Leu Lys Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu
          195          200          205
Thr Arg Val Asn Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe
          210          215          220
Asp Ala Thr Phe His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met
225          230          235          240
Leu Thr Lys Glu Leu Tyr Phe Tyr His
          245

```

<210> 9

<211> 147

<212> PRT

<213> Homo sapiens

<400> 9

```

Ser Gly Ile Ser Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met
 1           5           10           15
Gly Leu Cys Ile Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly
          20           25           30
Met Thr Ser Arg Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu
          35           40           45
Thr Phe Arg Asn Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr
          50           55           60
Arg Glu Glu Ile Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His
65           70           75           80
Ser Lys Arg Ser Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu

```

BEST AVAILABLE COPY

```

      85      90      95
Gly Ile Ile Phe Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr
      100      105      110
Asn Phe Phe Arg Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys
      115      120      125
Leu Phe Ile Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile
      130      135      140
Glu Thr Asp
145

```

<210> 10

<211> 102

<212> PRT

<213> Homo sapiens

<400> 10

```

Ser Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala
  1      5      10      15
Asp Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg
      20      25      30
Asn Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu
      35      40      45
Lys Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val
      50      55      60
Asn Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr
      65      70      75      80
Phe His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys
      85      90      95
Glu Leu Tyr Phe Tyr His
      100

```

BEST AVAILABLE COPY